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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/707,468A

DATE: 03/30/2001
 TIME: 15:44:51

Input Set : A:\Mor00031.app
 Output Set: N:\CRF3\03302001\I707468A.raw

ENTERED

3 <110> APPLICANT: Nicolaides, Nicholas C
 4 Grasso, Luigi
 5 Sass, Philip M
 7 <120> TITLE OF INVENTION: METHODS FOR GENERATING GENETICALLY ALTERED
 8 ANTIBODY-PRODUCING CELL LINES WITH IMPROVED ANTIIBODY
 9 CHARACTERISTICS
 11 <130> FILE REFERENCE: MOR-0003
 13 <140> CURRENT APPLICATION NUMBER: 09/707,468A
 14 <141> CURRENT FILING DATE: 2000-11-07
 16 <160> NUMBER OF SEQ ID NOS: 16
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 24
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
 27 primer
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 35 <212> TYPE: DNA
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 47 <211> LENGTH: 19
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
 53 primer
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 56 <221> NAME/KEY: misc_feature
 57 <222> LOCATION: (5)
 58 <223> OTHER INFORMATION: A or G or C or T/U
 60 <220> FEATURE:
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 62 <222> LOCATION: (11)
 63 <223> OTHER INFORMATION: A or G or C or T/U
 65 <400> SEQUENCE: 3 19
 W--> 66 akgtnmagct ncagsagtc
 69 <210> SEQ ID NO: 4

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70 <211> LENGTH: 19
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
76 primer
78 <220> FEATURE:
79 <221> NAME/KEY: misc_feature
80 <222> LOCATION: (2)
81 <223> OTHER INFORMATION: A or G or C or T/U
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88 <211> LENGTH: 859
89 <212> TYPE: PRT
90 <213> ORGANISM: Mus musculus
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94 1 5 10 15
96 Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile
97 20 25 30
99 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp
100 35 40 45
102 Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp
103 50 55 60
105 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Asn Phe
106 65 70 75 80
108 Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
109 85 90 95
111 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
112 100 105 110
114 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser
115 115 120 125
117 Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr
118 130 135 140
120 Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln
121 145 150 155 160
123 His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn
124 165 170 175
126 Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys
127 180 185 190
129 Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
130 195 200 205
132 Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys
133 210 215 220
135 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
136 225 230 235 240
138 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly
139 245 250 255

3/30/01

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142                260                265                270
144 Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser
145                275                280                285
147 Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser
148                290                295                300
150 Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
151 305                310                315                320
153 Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
154                325                330                335
156 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
157                340                345                350
159 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn
160                355                360                365
162 Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
163                370                375                380
165 Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln
166 385                390                395                400
168 Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala
169                405                410                415
171 Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu
172                420                425                430
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177 Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser
178                450                455                460
180 Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp
181 465                470                475                480
183 Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly
184                485                490                495
186 Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu
187                500                505                510
189 Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp
190                515                520                525
192 Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro
193                530                535                540
195 Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys
196 545                550                555                560
198 Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe
199                565                570                575
201 Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro
202                580                585                590
204 Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met
205                595                600                605
207 Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys
208                610                615                620
210 Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu
211 625                630                635                640
213 Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala

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214          645          650          655
216 Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu
217          660          665          670
219 Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu
220          675          680          685
222 Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr
223          690          695          700
225 Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu
226 705          710          715          720
228 Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu
229          725          730          735
231 Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile
232          740          745          750
234 Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro
235          755          760          765
237 Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile
238          770          775          780
240 Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val
241 785          790          795          800
243 Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly
244          805          810          815
246 Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly
247          820          825          830
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253          850          855
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257 <211> LENGTH: 3056
258 <212> TYPE: DNA
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261 <400> SEQUENCE: 6
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264 gtcttttccc gagagcggca ccgcaactct cccgcggtga ctgtgactgg aggagtccctg 180
265 catccatgga gcaaaccgaa ggcgtgagta cagaatgtgc taaggccatc aagcctattg 240
266 atgggaagtc agtccatcaa atttgttctg ggcaggtgat actcagttta agcaccgctg 300
267 tgaaggagtt gatagaaaat agtgtagatg ctggtgctac tactattgat ctaaggctta 360
268 aagactatgg ggtggacctc attgaagttt cagacaatgg atgtggggta gaagaagaaa 420
269 actttgaagg tctagctctg aaacatcaca catctaagat tcaagagttt gccgacctca 480
270 cgcaggttga aactttcggc tttcgggggg aagctctgag ctctctgtgt gcactaagtg 540
271 atgtcactat atctacctgc caccgggtctg caagcgttgg gactcgactg gtgtttgacc 600
272 ataatgggaa aatcacccag aaaactccct acccccgacc taaaggaacc acagtcagtg 660
273 tgcagcactt attttataca ctaccctgac gttacaaaga gtttcagagg aacattaaaa 720
274 aggagtattc caaaatggtg caggtcttac aggcgtactg tatcatctca gcaggcgtcc 780
275 gtgtaagctg cactaatcag ctcgacaggg ggaagcggca cgtgtgtgtg tgcacaagcg 840
276 gcacgtctgg catgaaggaa aatatcgggt ctgtgtttgg ccagaagcag ttgcaaagcc 900
277 tcattccttt tgttcagctg cccctagtgt acgctgtgtg tgaagagtac ggctgagca 960
278 cttcaggacg ccacaaaacc ttttctacgt ttcgggcttc atttcacagt gcacgcacgg 1020

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279 cgccgggagg agtgcaacag acaggcagtt tttcttcac aatcagaggc cctgtgaccc 1080
280 agcaaagggtc tctaagcttg tcaatgaggt tttatcacat gtataaccgg catcagtacc 1140
281 catttgctgt ccttaacgtt tccgttgact cagaatgtgt ggatattaat gtaactccag 1200
282 ataaaaggca aattctacta caagaagaga agctattgct ggccgtttta aagacctcct 1260
283 tgataggaat gtttgacagt gatgcaacaa agcttaatgt caaccagcag ccactgctag 1320
284 atgttggaagg taacttagta aagctgcata ctgcagaact agaaaagcct gtgccaggaa 1380
285 agcaagataa ctctccttca ctgaagagca cagcagacga gaaaagggtg gcatccatct 1440
286 ccaggctgag agaggccttt tctcttcac ctactaaaga gatcaagtct aggggtccag 1500
287 agactgctga actgacacgg agttttccaa gtgagaaaag gggcgtgtta tctctttatc 1560
288 ctccagacgt catctcttac agaggcctcc gtggctcgca ggacaaattg gtgagtecca 1620
289 cggacagccc tgggtgactgt atggacagag agaaaataga aaaagactca gggctcagca 1680
290 gcacctcagc tggtctgag gaagagttca gcaccccaga agtgggcagt agcttttagca 1740
291 gtgactataa cgtgagctcc ctagaagaca gaccttctca ggaaaccata aactgtgggtg 1800
292 acctggactg cgtcctctca ggtacaggac agtcttgaa gccagaagac catggatctc 1860
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311 tgatccgggtg ggagctcatg tgagcccagg actttgagac cactccgagc cacattcatg 3000
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315 <210> SEQ ID NO: 7

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317 <212> TYPE: PRT

318 <213> ORGANISM: Homo sapiens

320 <400> SEQUENCE: 7

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327 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp
328 35 40 45
330 Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
331 50 55 60
333 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
334 65 70 75 80

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L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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